



# 2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LITTMAN, DAN R.  
DENG, HONGKUI  
ELLMEIER, WILFRIED  
LANDAU, NATHANIEL R.  
LIU, RONG
- (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: David A. Jackson, Esq.
  - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/734,221
  - (B) FILING DATE: 2000/12/11
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/666,020
  - (B) FILING DATE: 19-JUN-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/227,319
  - (B) FILING DATE: 13-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Jackson Esq., David A.
  - (B) REGISTRATION NUMBER: 26,742
  - (C) REFERENCE/DOCKET NUMBER: 1049-1-004 N2
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGATCCG GTGGAACAAG ATGGATTAT

29

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGTCGACA TGTGCACAAC TCTGACTG

28

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC 60  
CAAAAA 66

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr  
1                      5                      10                      15  
Ser Glu Pro Cys Gln Lys  
                    20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCAGAT 60  
TATGCTTCGG AGCCCTGCCA AAAA 84

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Pro	Tyr
1				5					10					15	

Asp	Val	Pro	Asp	Tyr	Ala	Ser	Glu	Pro	Cys	Gln	Lys
			20					25			

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A

51

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 63 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGGATCCA CCATGGATTA TCAAGTGTCA AGTCCAATCT ATGACATCAA TTATCCATAC 60

GAT 63

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATACGATG TTCCAGATTA TGCT 24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATACG ATGTTCCAGA TTATGCTTCG

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAGATGGAT	60
TATCAAGTGT CAAGTCCAAT CTATGACATC AATTATTATA CATCGGAGCC CTGCCAAAAA	120
ATCAATGTGA AGCAAATCGC AGCCCGCCTC CTGCCTCCGC TCTACTCACT GGTGTTTCATC	180
TTTGGTTTTG TGGGCAACAT GCTGGTCATC CTCATCCTGA TAAACTGCAA AAGGCTGAAG	240
AGCATGACTG ACATCTACCT GCTCAACCTG GCCATCTCTG ACCTGTTTTT CCTTCTTACT	300
GTCCCCTTCT GGGCTCACTA TGCTGCCGCC CAGTGGGACT TTGGAAATAC AATGTGTCAA	360
CTCTTGACAG GGCTCTATTT TATAGGCTTC TTCTCTGGAA TCTTCTTCAT CATCCTCCTG	420
ACAATCGATA GGTACCTGGC TGTCGTCCAT GCTGTGTTTG CTTTAAAAGC CAGGACGGTC	480
ACCTTTGGGG TGGTGACAAG TGTGATCACT TGGGTGGTGG CTGTGTTTGC GTCTCTCCCA	540
GGAATCATCT TTACCAGATC TCAAAAAGAA GGTCTTCATT ACACCTGCAG CTCTCATTTT	600
CCATACAGTC AGTATCAATT CTGGAAGAAT TTCCAGACAT TAAAGATAGT CATCTTGGGG	660
CTGGTCCTGC CGCTGCTTGT CATGGTCATC TGCTACTCGG GAATCCTAAA AACTCTGCTT	720
CGGTGTCGAA ATGAGAAGAA GAGGCACAGG GCTGTGAGGC TTATCTTCAC CATCATGATT	780
GTTTATTTTC TCTTCTGGGC TCCCTACAAC ATTGTCCTTC TCCTGAACAC CTTCCAGGAA	840
TTCTTTGGCC TGAATAATTG CAGTAGCTCT AACAGGTTGG ACCAAGCTAT GCAGGTGACA	900
GAGACTCTTG GGATGACGCA CTGCTGCATC AACCCCATCA TCTATGCCTT TGTCGGGGAG	960
AAGTTCAGAA ACTACCTCTT AGTCTTCTTC CAAAAGCACA TTGCCAAACG CTTCTGCAAA	1020
TGCTGTTCTA TTTTCCAGCA AGAGGCTCCC GAGCGAGCAA GCTCAGTTTA CACCCGATCC	1080
ACTGGGGAGC AGGAAATATC TGTGGGCTTG TGACACGGAC TCAAGTGGGC TGGTGACCCA	1140
GTCAGAGTTG TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGGA	1200
GAGGTCTTTT TTAAAAGGAA GTTACTGTTA TAGAGGGTCT AAGATTCATC CATTTATTTG	1260
GCATCTGTTT AAAGTAGATT AGATCTTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAA	1320
ATATGTTGAT GAAAAATAGC AACCTTTTTA TCTCCCCTTC ACATGCATCA AGTTATTGAC	1380
AAACTCTCCC TTTACTCCGA AAGTTCCTTA TGTATATTTA AAAGAAAGCC TCAGAGAATT	1440
GCTGATTCTT GAGTTTAGTG ATCTGAACAG AAATACCAAA ATTATTTTCTAG AAATGTACAA	1500
CTTTTTACCT AGTACAAGGC AACATATAGG TTGTAAATGT GTTTAAAACA GGTCTTTGTC	1560
TTGCTATGGG GAGAAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCATGTGTG	1620
ATTTCCCCTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCAGGC GAGAGACTTG	1680

TGGCCTGGGA	GAGCTGGGGA	AGCTTCTTAA	ATGAGAAGGA	ATTTGAGTTG	GATCATCTAT	1740
TGCTGGCAAA	GACAGAAGCC	TCAGTCAAG	CACTGCATGG	GCAAGCTTGG	CTGTAGAAGG	1800
AGACAGAGCT	GGTTGGGAAG	ACATGGGGAG	GAAGGACAAG	GCTAGATCAT	GAAGAACCTT	1860
GACGGCATTG	CTCCGTCTAA	GTCATGAGCT	GAGCAGGGAG	ATCCTGGTTG	GTGTTGCAGA	1920
AGGTTTACTC	TGTGGCCAAA	GGAGGGTCAG	GAAGGATGAG	CATTTAGGGC	AAGGAGACCA	1980
CCAACAGCCC	TCAGGTCAGG	GTGAGGATGG	CCTCTGCTAA	GCTCAAGGCG	TGAGGATGGG	2040
AAGGAGGGAG	GTATTCGTAA	GGATGGGAAG	GAGGGAGGTA	TTCGTGCAGC	ATATGAGGAT	2100
GCAGAGTCAG	CAGAACTGGG	GTGGATTTGG	TTTGGAAGTG	AGGGTCAGAG	AGGAGTCAGA	2160
GAGAATCCCT	AGTCTTCAAG	CAGATTGGAG	AAACCCCTGA	AAAGACATCA	AGCACAGAAG	2220
GAGGAGGAGG	AGGTTTAGGT	CAAGAAGAAG	ATGGATTGGT	GTAAAAGGAT	GGGTCTGGTT	2280
TGCAGAGCTT	GAACACAGTC	TCACCCAGAC	TCCAGGCTGT	CTTTCACTGA	ATGCTTCTGA	2340
CTTCATAGAT	TTCCTTCCCA	TCCCAGCTGA	AATACTGAGG	GGTCTCCAGG	AGGAGACTAG	2400
ATTTATGAAT	ACACGAGGTA	TGAGGTCTAG	GAACATACTT	CAGCTCACAC	ATGAGATCTA	2460
GGTGAGGATT	GATTACCTAG	TAGTCATTTT	ATGGGTTGTT	GGGAGGATTC	TATGAGGCAA	2520
CCACAGGCAG	CATTTAGCAC	ATACTACACA	TTCAATAAGC	ATCAAACTCT	TAGTTACTCA	2580
TTCAGGGATA	GCACTGAGCA	AAGCATTGAG	CAAAGGGGTC	CCATATAGGT	GAGGGAAGCC	2640
TGAAAAACTA	AGATGCTGCC	TGCCCAGTGC	ACACAAGTGT	AGGTATCATT	TTCTGCATTT	2700
AACCGTCAAT	AGGCAAAGGG	GGGAAGGGAC	ATATTCATTT	GGAAATAAGC	TGCCTTGAGC	2760
CTTAAAACCC	ACAAAAGTAC	AATTTACCAG	CCTCCGTATT	TCAGACTGAA	TGGGGGTGGG	2820
GGGGGCGCCT	TAGGTACTTA	TTCCAGATGC	CTTCTCCAGA	CAAACCAGAA	GCAACAGAAA	2880
AAATCGTCTC	TCCCTCCCTT	TGAAATGAAT	ATACCCCTTA	GTGTTTGGGT	ATATTCATTT	2940
CAAAGGGAGA	GAGAGAGGTT	TTTTTCTGTT	CTTTCTCATA	TGATTGTGCA	CATACTTGAG	3000
ACTGTTTTGA	ATTTGGGGGA	TGGCTAAAAC	CATCATAGTA	CAGGTAAGGT	GAGGGAATAG	3060
TAAGTGGTGA	GAAGTACTCA	GGGAATGAAG	GTGTCAGAAT	AATAAGAGGT	GCTACTGACT	3120
TTCTCAGCCT	CTGAATATGA	ACGGTGAGCA	TTGTGGCTGT	CAGCAGGAAG	CAACGAAGGG	3180
AAATGTCTTT	CCTTTTGCTC	TTAAGTTGTG	GAGAGTGCAA	CAGTAGCATA	GGACCCTACC	3240
CTCTGGGCCA	AGTCAAAGAC	ATTCTGACAT	CTTAGTATTT	GCATATTCTT	ATGTATGTGA	3300
AAGTTACAAA	TTGCTTGAAA	GAAAATATGC	ATCTAATAAA	AAACACCTTC	TAAAATAAAA	3360



(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	1	5	10	15
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	20	25	30	
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	35	40	45	
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	50	55	60	
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	65	70	75	80
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	85	90	95	
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	100	105	110	
Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	115	120	125	
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	130	135	140	
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	145	150	155	160
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	165	170	175	
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	180	185	190	

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
 195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
 210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
 225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
 245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
 260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
 275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
 290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
 305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
 325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
 340 345 350